

SEQUENCE LISTING

<110> Bandaru, Rajasekhar
Meyers, Rachel A.

<120> 55562 AND 21617, NOVEL HUMAN PROTEINS
AND METHODS OF USE THEREOF

<130> 10448-123001

<150> 60/256,249

<151> 2000-12-18

<150> 60/256,405

<151> 2000-12-18

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3624

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (339)...(1361)

<400> 1

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ccggggccac agcgcgcgag ccgggcggga gtggccccgc gcaggcaggg agcggcgccg      180
cgcaactccaa cccggcgggc acctcggggg cgggcgcggg gcgcagcctt ctggtcccgg      240
cctctgtgac aagcgccccg gagccgggag cccgattgcc gggctcgggg tgggcgcgga      300
cgcaggcact gggctcgtgc ggggcccccg gcgtcgcg atg aac atc gtg gtg gag      356
                               Met Asn Ile Val Val Glu
                               1             5

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ttc ttc gtg gtc act ttc aaa gtg ctc tgg gcg ttc gtg ctg gcc gcg      404
Phe Phe Val Val Thr Phe Lys Val Leu Trp Ala Phe Val Leu Ala Ala
          10             15             20

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gcg cgc tgg ctg gtg cgg ccc aag gag aag agc gtg gcg ggc cag gtg      452
Ala Arg Trp Leu Val Arg Pro Lys Glu Lys Ser Val Ala Gly Gln Val
          25             30             35

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tgc ctc atc acc ggc gcc ggc agc ggc ctg ggc cgc ctc ttc gcg ctg      500
Cys Leu Ile Thr Gly Ala Gly Ser Gly Leu Gly Arg Leu Phe Ala Leu
          40             45             50

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gag ttc gcc cgg cgt cgg gcg ctg ctg gtg ctg tgg gac atc aac acg      548
Glu Phe Ala Arg Arg Arg Ala Leu Leu Val Leu Trp Asp Ile Asn Thr
          55             60             65             70

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caa agc aac gag gag acg gct ggc atg gtg cgc cac atc tac cgc gac	596
Gln Ser Asn Glu Glu Thr Ala Gly Met Val Arg His Ile Tyr Arg Asp	
75 80 85	
ctg gag gcg gcc gac gcc gct gcg ctg caa gct ggg aat ggt gag gaa	644
Leu Glu Ala Ala Asp Ala Ala Ala Leu Gln Ala Gly Asn Gly Glu Glu	
90 95 100	
gaa att ctg ccc cac tgt aac ttg cag gtt ttt acc tac acc tgt gac	692
Glu Ile Leu Pro His Cys Asn Leu Gln Val Phe Thr Tyr Thr Cys Asp	
105 110 115	
gtg ggg aag agg gag aac gtc tac ctg acg gct gaa aga gtc cgc aag	740
Val Gly Lys Arg Glu Asn Val Tyr Leu Thr Ala Glu Arg Val Arg Lys	
120 125 130	
gag gtt ggc gaa gtc tca gtc ctg gtc aat aat gct ggt gtg gtc tct	788
Glu Val Gly Glu Val Ser Val Leu Val Asn Asn Ala Gly Val Val Ser	
135 140 145 150	
ggg cat cac ctt ctg gaa tgt cct gat gag ctc att gag aga acc atg	836
Gly His His Leu Leu Glu Cys Pro Asp Glu Leu Ile Glu Arg Thr Met	
155 160 165	
atg gtc aat tgc cat gca cac ttc tgg acc act aag gct ttt ctt cct	884
Met Val Asn Cys His Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro	
170 175 180	
acg atg ctg gag att aat cat ggt cat att gtg aca gtt gca agt tcc	932
Thr Met Leu Glu Ile Asn His Gly His Ile Val Thr Val Ala Ser Ser	
185 190 195	
ttg gga ttg ttc agt act gcc gga gtt gag gat tac tgt gcc agt aaa	980
Leu Gly Leu Phe Ser Thr Ala Gly Val Glu Asp Tyr Cys Ala Ser Lys	
200 205 210	
ttt gga gtt gtg ggt ttt cat gaa tcc ctg agc cat gaa cta aag gct	1028
Phe Gly Val Val Gly Phe His Glu Ser Leu Ser His Glu Leu Lys Ala	
215 220 225 230	
gct gaa aag gat gga att aaa aca acc ttg gtt tgc cct tat ctt gta	1076
Ala Glu Lys Asp Gly Ile Lys Thr Thr Leu Val Cys Pro Tyr Leu Val	
235 240 245	
gac act ggc atg ttc aga ggc tgc cga atc agg aaa gaa att gag cct	1124
Asp Thr Gly Met Phe Arg Gly Cys Arg Ile Arg Lys Glu Ile Glu Pro	
250 255 260	
ttt ctg cca cct ctg aag cct gat tac tgt gtg aag cag gcc atg aag	1172
Phe Leu Pro Pro Leu Lys Pro Asp Tyr Cys Val Lys Gln Ala Met Lys	
265 270 275	
gcc atc ctc act gac cag ccc atg atc tgc act ccc cgc ctc atg tac	1220
Ala Ile Leu Thr Asp Gln Pro Met Ile Cys Thr Pro Arg Leu Met Tyr	
280 285 290	
atc gtg acc ttc atg aag agc atc cta cca ttt gaa gca gtt gtg tgc	1268

Ile Val Thr Phe Met Lys Ser Ile Leu Pro Phe Glu Ala Val Val Cys
 295 305 310

atg tat cgg ttc cta gga gcg gac aag tgt atg tac ccc ttt att gct 1316
 Met Tyr Arg Phe Leu Gly Ala Asp Lys Cys Met Tyr Pro Phe Ile Ala
 315 320 325

caa aga aag caa gcc aca aac aat aat gaa gca aaa aat gga atc 1361
 Gln Arg Lys Gln Ala Thr Asn Asn Asn Glu Ala Lys Asn Gly Ile
 330 335 340

taagaatctt tttgtatgga atattacttc tatcagaaga tgatcaagat gtttcagtcc 1421
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<210> 2

<211> 341

<212> PRT

<213> Homo sapiens

<400> 2

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Ser Val Ala Gly Gln Val Cys Leu Ile Thr Gly Ala Gly Ser Gly Leu			
35	40	45	
Gly Arg Leu Phe Ala Leu Glu Phe Ala Arg Arg Arg Ala Leu Leu Val			
50	55	60	
Leu Trp Asp Ile Asn Thr Gln Ser Asn Glu Glu Thr Ala Gly Met Val			
65	70	75	80
Arg His Ile Tyr Arg Asp Leu Glu Ala Ala Asp Ala Ala Ala Leu Gln			
85	90	95	
Ala Gly Asn Gly Glu Glu Glu Ile Leu Pro His Cys Asn Leu Gln Val			
100	105	110	
Phe Thr Tyr Thr Cys Asp Val Gly Lys Arg Glu Asn Val Tyr Leu Thr			
115	120	125	
Ala Glu Arg Val Arg Lys Glu Val Gly Glu Val Ser Val Leu Val Asn			
130	135	140	
Asn Ala Gly Val Val Ser Gly His His Leu Leu Glu Cys Pro Asp Glu			
145	150	155	160
Leu Ile Glu Arg Thr Met Met Val Asn Cys His Ala His Phe Trp Thr			
165	170	175	
Thr Lys Ala Phe Leu Pro Thr Met Leu Glu Ile Asn His Gly His Ile			
180	185	190	
Val Thr Val Ala Ser Ser Leu Gly Leu Phe Ser Thr Ala Gly Val Glu			
195	200	205	
Asp Tyr Cys Ala Ser Lys Phe Gly Val Val Gly Phe His Glu Ser Leu			
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Ser His Glu Leu Lys Ala Ala Glu Lys Asp Gly Ile Lys Thr Thr Leu			
225	230	235	240
Val Cys Pro Tyr Leu Val Asp Thr Gly Met Phe Arg Gly Cys Arg Ile			
245	250	255	
Arg Lys Glu Ile Glu Pro Phe Leu Pro Pro Leu Lys Pro Asp Tyr Cys			
260	265	270	
Val Lys Gln Ala Met Lys Ala Ile Leu Thr Asp Gln Pro Met Ile Cys			
275	280	285	
Thr Pro Arg Leu Met Tyr Ile Val Thr Phe Met Lys Ser Ile Leu Pro			
290	295	300	
Phe Glu Ala Val Val Cys Met Tyr Arg Phe Leu Gly Ala Asp Lys Cys			
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Met Tyr Pro Phe Ile Ala Gln Arg Lys Gln Ala Thr Asn Asn Asn Glu			
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<210> 3

<211> 1026

<212> DNA

<213> Homo sapiens

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atcaccggcg	ccggcagcgg	cctgggcccgc	ctcttcgcgc	tgagtttcgc	ccggcgctcg	180
gcgctgctgg	tgctgtggga	catcaacacg	caaagcaacg	aggagacggc	tggtcatggtg	240
cgccacatct	accgcgacct	ggaggcggcc	gacgccgctg	cgctgcaagc	tggggaatggt	300
gaggaagaaa	ttctgccccca	ctgtaacttg	caggttttta	cctacacctg	tgacgtgggg	360
aagagggaga	acgtctacct	gacggctgaa	agagtccgca	aggaggttgg	cgaagtctca	420

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gtcctggtca ataatgctgg tgtggtctct gggcatcacc ttctggaatg tcctgatgag 480
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cttcctacga tgctggagat taatcatggt catattgtga cagttgcaag ttccttgga 600
ttgttcagta ctgccggagt tgaggattac tgtgccagta aatttgaggt tgtgggtttt 660
catgaatccc tgagccatga actaaaggct gctgaaaagg atggaattaa aacaaccttg 720
gtttgccctt atcttgtaga cactggcatg ttcagaggct gccgaatcag gaaagaaatt 780
gagccttttc tgccacctct gaagcctgat tactgtgtga agcaggccat gaaggccatc 840
ctcactgacc agcccatgat ctgcactccc cgcctcatgt acatcgtgac cttcatgaag 900
agcatcctac catttgaagc agttgtgtgc atgtatcggg tcctaggagc ggacaagtgt 960
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<211> 1327

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<222> (367)...(1188)

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cggatacacc ttgcgaagaa tgcgcactc tccgccactc attccccact caccggcacc 180
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agtgtacac tcaaagcctg ccgtcgcagt gagcgcgacc tccaaactga ggcatttttg 300
ttccggcgaa atccctccca ctcaggaaag tccctagaaa gagagcgcag ggcgcctggg 360
tatcac atg acc act tcc cgg aag cgc agc aga ccc gct caa ctt cat 408
      Met Thr Thr Ser Arg Lys Arg Ser Arg Pro Ala Gln Leu His
        1             5             10

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cct ggg ttg agg cgg agg aga act tcc aga att atg gcg aag tcc ggg 456
Pro Gly Leu Arg Arg Arg Arg Thr Ser Arg Ile Met Ala Lys Ser Gly
  15             20             25             30

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ctg agg cag gac ccg cag agc aca gct gca gcc act gtg cta aag cgg 504
Leu Arg Gln Asp Pro Gln Ser Thr Ala Ala Ala Thr Val Leu Lys Arg
          35             40             45

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gca gta gaa cta gat tcg gag tcg cgg tat ccg cag gct ctg gtg tgt 552
Ala Val Glu Leu Asp Ser Glu Ser Arg Tyr Pro Gln Ala Leu Val Cys
      50             55             60

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tac caa gag ggg att gat ctg ctc ctg cag gtt ctg aaa ggt acc aaa 600
Tyr Gln Glu Gly Ile Asp Leu Leu Leu Gln Val Leu Lys Gly Thr Lys
      65             70             75

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gat aat act aag aga tgt aat ctc aga gaa aaa att tcc aaa tac atg 648
Asp Asn Thr Lys Arg Cys Asn Leu Arg Glu Lys Ile Ser Lys Tyr Met
      80             85             90

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gac aga gcg gaa aac ata aag aag tac ttg gac caa gaa aaa gaa gat 696
Asp Arg Ala Glu Asn Ile Lys Lys Tyr Leu Asp Gln Glu Lys Glu Asp
      95             100             105             110

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gga aaa tat cac aag caa att aaa ata gaa gag aat gca aca ggt ttc 744

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Gly Lys Tyr His Lys Gln Ile Lys Ile Glu Glu Asn Ala Thr Gly Phe
 115 120 125
 agt tat gag tca ctt ttt cgc gaa tac ctt aat gag aca gtt aca gaa 792
 Ser Tyr Glu Ser Leu Phe Arg Glu Tyr Leu Asn Glu Thr Val Thr Glu
 130 135 140
 gtt tgg ata gaa gat cct tat att aga cat act cat cag ctg tat aac 840
 Val Trp Ile Glu Asp Pro Tyr Ile Arg His Thr His Gln Leu Tyr Asn
 145 150 155
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 Phe Leu Arg Phe Cys Glu Met Leu Ile Lys Arg Pro Cys Lys Val Lys
 160 165 170
 act att cac ctt ctc acc tct ctg gat gaa ggc att gag caa gtg cag 936
 Thr Ile His Leu Leu Thr Ser Leu Asp Glu Gly Ile Glu Gln Val Gln
 175 180 185 190
 caa agt aga ggc ctg caa gaa ata gaa gag tca ctc agg agt cac gga 984
 Gln Ser Arg Gly Leu Gln Glu Ile Glu Glu Ser Leu Arg Ser His Gly
 195 200 205
 gtg ctg ttg gaa gtt caa tac tct tct tca ata cat gac cga gaa att 1032
 Val Leu Leu Glu Val Gln Tyr Ser Ser Ser Ile His Asp Arg Glu Ile
 210 215 220
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 Arg Phe Asn Asn Gly Trp Met Ile Lys Ile Gly Arg Gly Leu Asp Tyr
 225 230 235
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 Phe Lys Lys Pro Gln Ser Arg Phe Ser Leu Gly Tyr Cys Asp Phe Asp
 240 245 250
 tta aga cca tgt cat gaa aca aca gta gac att ttt cat aag aag cat 1176
 Leu Arg Pro Cys His Glu Thr Thr Val Asp Ile Phe His Lys Lys His
 255 260 265 270
 aca aaa aat ata tgatgggtgg tagcctaatt tgtattatgt ctactttaag 1228
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<210> 5

<211> 274

<212> PRT

<213> Homo sapiens

<400> 5

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 Leu Arg Arg Arg Arg Thr Ser Arg Ile Met Ala Lys Ser Gly Leu Arg
 20 25 30
 Gln Asp Pro Gln Ser Thr Ala Ala Ala Thr Val Leu Lys Arg Ala Val

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      35              40              45
Glu Leu Asp Ser Glu Ser Arg Tyr Pro Gln Ala Leu Val Cys Tyr Gln
  50              55              60
Glu Gly Ile Asp Leu Leu Gln Val Leu Lys Gly Thr Lys Asp Asn
  65              70              75              80
Thr Lys Arg Cys Asn Leu Arg Glu Lys Ile Ser Lys Tyr Met Asp Arg
      85              90              95
Ala Glu Asn Ile Lys Lys Tyr Leu Asp Gln Glu Lys Glu Asp Gly Lys
      100              105              110
Tyr His Lys Gln Ile Lys Ile Glu Glu Asn Ala Thr Gly Phe Ser Tyr
      115              120              125
Glu Ser Leu Phe Arg Glu Tyr Leu Asn Glu Thr Val Thr Glu Val Trp
      130              135              140
Ile Glu Asp Pro Tyr Ile Arg His Thr His Gln Leu Tyr Asn Phe Leu
      145              150              155              160
Arg Phe Cys Glu Met Leu Ile Lys Arg Pro Cys Lys Val Lys Thr Ile
      165              170              175
His Leu Leu Thr Ser Leu Asp Glu Gly Ile Glu Gln Val Gln Gln Ser
      180              185              190
Arg Gly Leu Gln Glu Ile Glu Glu Ser Leu Arg Ser His Gly Val Leu
      195              200              205
Leu Glu Val Gln Tyr Ser Ser Ile His Asp Arg Glu Ile Arg Phe
      210              215              220
Asn Asn Gly Trp Met Ile Lys Ile Gly Arg Gly Leu Asp Tyr Phe Lys
      225              230              235              240
Lys Pro Gln Ser Arg Phe Ser Leu Gly Tyr Cys Asp Phe Asp Leu Arg
      245              250              255
Pro Cys His Glu Thr Thr Val Asp Ile Phe His Lys Lys His Thr Lys
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Asn Ile

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<210> 6
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<212> DNA
<213> Homo sapiens

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gccactgtgc taaagcgggc agtagaacta gattcggagt cgcggtatcc gcaggctctg      180
gtgtgttacc aagaggggat tgatctgctc ctgcagggtt tgaaaggtac caaagataat      240
actaagagat gtaatctcag agaaaaaatt tccaaataca tggacagagc ggaaaacata      300
aagaagtact tggaccaaga aaaagaagat ggaaaatatc acaagcaa ataaatagaa      360
gagaatgcaa caggtttcag ttatgagtca ctttttcgcg aataccttaa tgagacagtt      420
acagaagttt ggatagaaga tccttatatt agacatactc atcagctgta taactttctt      480
cgattttgtg agatgcttat taagagacca tgtaaagtaa aaactattca ctttctcacc      540
tctctggatg aaggcattga gcaagtgcag caaagtagag gcctgcaaga aatagaagag      600
tactcagga gtcacggagt gctgttgga gttcaatact cttcttcaat acatgaccga      660
gaaattaggt tcaacaatgg atggatgatt aagattggaa ggggacttga ttattttaag      720
aaaccacaga gtcgtttttc ccttgatat tgtgattttg atttaagacc atgtcatgaa      780
acaacagtag acattttttc taagaagcat acaaaaaata tatga      825

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<210> 7
<211> 206
<212> PRT
<213> Artificial Sequence

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<220>

<223> Consensus sequence

<400> 7

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Lys Val Ala Leu Val Thr Gly Ala Ser Ser Gly Ile Gly Leu Ala Ile
 1           5           10          15
Ala Lys Arg Leu Ala Lys Glu Gly Ala Lys Val Val Val Ala Asp Arg
          20          25          30
Asn Glu Glu Lys Leu Glu Lys Gly Ala Val Ala Lys Glu Leu Lys Glu
          35          40          45
Leu Gly Gly Asn Asp Lys Asp Arg Ala Leu Ala Ile Gln Leu Asp Val
          50          55          60
Thr Asp Glu Glu Ser Val Lys Ala Ala Val Glu Gln Ala Val Glu Arg
65          70          75          80
Leu Gly Arg Gly Leu Asp Val Leu Val Asn Asn Ala Gly Gly Ile Ile
          85          90          95
Leu Leu Arg Pro Gly Pro Phe Ala Glu Leu Ser Arg Thr Met Glu Glu
          100         105         110
Asp Trp Asp Arg Val Ile Asp Val Asn Leu Thr Gly Val Phe Leu Leu
          115         120         125
Thr Arg Ala Val Leu Pro Leu Met Ala Met Lys Lys Arg Gly Gly Gly
          130         135         140
Arg Ile Val Asn Ile Ser Ser Val Ala Gly Arg Lys Glu Gly Gly Leu
          145         150         155         160
Val Gly Val Pro Gly Gly Ser Ala Tyr Ser Ala Ser Lys Ala Ala Val
          165         170         175
Ile Gly Leu Thr Arg Ser Leu Ala Leu Glu Leu Ala Pro His Gly Gly
          180         185         190
Ile Arg Val Asn Ala Val Ala Pro Gly Gly Val Asp Thr Asp
          195         200         205

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<210> 8

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 8

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Ala Glu Ala Tyr Tyr Asn Leu Gly Asn Ala Tyr Leu Lys Leu Gly Lys
 1           5           10          15
Tyr Asp Glu Ala Ile Glu Asp Tyr Glu Lys Ala Leu Glu Leu Asp Pro
          20          25          30
Asn Asn

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<210> 9

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 9

Ala Lys Glu Leu Leu Ile Arg Ala Val Glu Cys Asp Gln Val' Gly Arg
 1 5 10 15
 Ile Leu Glu Ala Gln Thr Leu Tyr Thr Glu Gly Ile Gly Gln Leu Met
 20 25 30
 Gln Phe Val Asn Gly Glu Pro Asp Glu Ala Lys Arg Lys Gly Phe Leu
 35 40 45
 Thr Arg Ile Lys Glu Tyr Met Asp Arg Ala Asp Ala Ile Lys Ala Arg
 50 55 60
 Ile Asn Gly Lys Leu Met Leu Gly Glu Val Val Ser His Val Ser Ile
 65 70 75 80
 Asp Glu Asn Asp Thr Gly Phe Asp Tyr Asp Gln Leu Phe Gly Lys Tyr
 85 90 95
 Met Asp Asp Lys Thr Val Glu Ile Met Leu Glu Glu Pro Tyr Met Thr
 100 105 110
 Gln Asn Tyr Gln Tyr Gln Asn Leu Ile Arg Phe Leu Glu Leu Ala Ala
 115 120 125
 Thr Asn Cys Pro Asn Leu Lys Tyr Phe Arg Leu Ile Thr Lys Glu Tyr
 130 135 140
 Lys Asp Ala Lys Asn Pro Asp Gln Gln Glu Thr Asn Leu Gly Gln Ile
 145 150 155 160
 Lys Gly Asp Leu Glu Arg Arg Asn Val Thr Val Tyr Ile Lys Tyr Glu
 165 170 175
 Asp Ser Leu His Asp Arg Lys Ile Tyr Leu Ser Asn Gly Tyr Ile Ile
 180 185 190
 Lys Ile Gly Arg Gly Leu His Phe Tyr Lys Pro Ala Asn Pro Met Tyr
 195 200 205
 Ser Ile Gly Leu Val Asn Tyr Lys Phe Arg Lys Cys Leu Gln Thr Asp
 210 215 220
 Val Asp Ile Trp
 225

<210> 10

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 10

Ala Ile Asp Leu Val Gln Lys Ala Ile Asp Glu Asp Lys Ala Gly Gln
 1 5 10 15
 Tyr Glu Glu Ala Tyr Gln Leu Tyr Gln His Ala Leu Asp Tyr Phe Met
 20 25 30
 His Ala Leu Lys Tyr Glu Ala Lys Asn Asp Lys Ser Lys Glu Ile Ile
 35 40 45
 Arg Ala Lys Cys Thr Glu Tyr Leu Asp Arg Ala
 50 55